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LOCUS       AF114024             357 bp      mRNA              INV          27-JAN-2000
DEFINITION  Buthus martensii neurotoxin P01 (P01) mRNA, complete cds.
ACCESSION   AF114024
VERSION     AF114024.1   GI:6690265
KEYWORDS    .
SOURCE      Chinese scorpion.
  ORGANISM  Buthus martensii
            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
            Buthoidea; Buthidae; Buthus.
REFERENCE   1  (bases 1 to 357)
  AUTHORS   Zhu,S.-Y., Zeng,X.-C., Li,W.-X. and Jiang,D.-H.
  TITLE     Molecular characterization of a K+ channel blocker from Buthus
            martensii
  JOURNAL   Chin. Sci. Bull. 44 (21), 2295-2299 (1999)
REFERENCE   2  (bases 1 to 357)
  AUTHORS   Zhu,S.-Y., Zeng,X.-C., Li,W.-X. and Jiang,D.-H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-DEC-1998) Virology, Life Science, Luojia Mountain,
            Wuhan, Hubei 430072, China
FEATURES             Location/Qualifiers
     source            1. .357
                       /organism="Buthus martensii"
                       /db_xref="taxon:34649"
                       /tissue_type="venom gland"
                       /note="synonym: Mesobuthus martensii; authority: Buthus
                       martensii Karsch"
     gene              1. .357
                       /gene="P01"
     CDS               68. .241
                       /gene="P01"
                       /function="potassium ion channel blocker"
                       /codon_start=1
                       /product="neurotoxin P01"
                       /protein_id="AAF24057.1"
                       /db_xref="GI:6690266"
                       /translation="MSRLYAIILIALVFNVIMTIIIPDMKVEAATCEDCPEHCATQNR
                       AKCDNDKCVCEPK"
BASE COUNT    156 a      68 c      60 g      73 t
ORIGIN

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Quality:	110.00	Length:	57
Ratio:	2.444	Gaps:	3
Percent Similarity:	78.947	Percent Identity:	43.860

US-09-599-416-2 x AF114024 ..

Align seg 1/1 to: AF114024 from: 1 to: 357

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1 MetSerArgIlePheThrIleIleLeuIleValPheAlaLeuAsnIleIl 17
  |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||: 17
68 ATGAGTCGACTTTATGCAATCATCTTAATTGCTCTTGTCTTCAATGTGAT 117

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17 eIleSer...LeuSerAsnPheLysValGluAlaAlaGlnCysTyrSerS 33
|:::  ::  :::::|||||||  ||  :
118 TATGACGATTATACCCGATATGAAAGTAGAGGCTGCTACCTGT.....G 161

33 erAspCysArgValLysCysAlaAlaMetGlyPheAsnSerGlyLysCys 49
::|  ||  |||||:::  :::  |||||
162 AAGATTGCCCCGAGCACTGTGCCACACAGAATGCCCGAGCA...AAATGC 208

50 IleAsnSerLysCysLysCys 56
|||::|  ||  |||
209 GATAATGACAAATGCGTATGT 229

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